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Maximum Match 100%
Listing first 45 summaries
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10137.587 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

2 (bases 1 to 6486) Pekarsky,Y., Hallas,C. and Croce,C.M.

MEDLINE REFERENCE AUTHORS	JOURNAL	REFERENCE AUTHORS TITLE	SOURCE ORGANISM	ACCESSION VERSION KEYWORDS	RESULT 1 AF110465 LOCUS DEFINITION		45 4	4.	4.4	40 45	4.4	37	ъ. #	ω ι 1 4 1	ъ л	31 46	46	46	į	24 46 25 46	46	21 47 22	47	18 49	<u>.</u>	15	57	64	701	701	701	1338	1633	C L	1	Result No. Score
99178995 2 (bases 1 to 6486) Pekarsky,Y., Hallas,C. and Croce,C.M.	oncogenes Proc. Natl. Acad. Sci. U.S.A. 96 (6), 29	Hallas,C., Isobe,M., Russo at 14q32.1 in T cell mali	apiens ota; Metazoa; Chordata; Craniata; ia; Eutheria; Primates; Catarrhini	AF110465 AF110465.1 GI:4324702	110465 6486 bp DNA go sapiens T-cell leukemia/lymphoma lE	ALIGNMENTS	6.8 172800 2	9 157756 9 8 97078 9	6.9 199287 2	6.9 179260 2 6 9 212656 9	7.0 157086 9	7.0 212656 9	7.0 176051 9	7.0 145631 2	7.1 171523 2 7.0 211544 9	7.1 206836 2	7.1 150036 9	7.1 100732 9	7.2 120766 9	7.2 1928/6 2 7.2 145442 9	7.2 186497 2	7.3 172757 2 7.3 173185 2	7.4 174095 2	7.6 137808 2	7.8 204843 9 7.7 1248 9	7.8 114438 2	8.8 627 9 AB025272S	9.9 753 9	10.8 3599 9	10.8 3240 9 10.8 3532 9	10.8 3144 9	10 8 1152 9	25.2 1717 9	و و	6486 9	Query Match Length DB I
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/protein_id="AAD16996.1"
/db_xref="GI:4324703"
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/taanslation="MASEASVRLGVPPGRLWIORPGIYEDEEGRTWVTVVVRFNPSRREWARASQGSRYEPSITVHLWQMAVHTRELLSSGQMPFSQLPAVWQLYPGRKYRAADSS
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2880	ctactaaaaatacaaaagaattagcogggtgcggtgggggggtctgtagtcccagctac	2821	γOγ
82	GGCGGATCACAAGGTCAGGAGATCGAGACCATCCTGGCTAACACGGTGAAACCCCGTCT	7	ממ
2820	ancadatcacaagatcagagatcagagacatcatagatcctagattaacacgatgaaaaccatc	2761	Ο _Ψ ξ
76	aaacagttgacogggcacggtggctcacggctgaatccccagcacttttgggggaccgaggc	1 7	2y
2700	CAATGCACTTAATGCCACCAAACTGTACTCTTA	2641	Дb
2700	ggatagtgccgacggttccacatgtcaatgcacttaatgccaccaaactgtactc	2641	Qy
2640 2640	gaagitaatgitagiaacaggiacggagitcicagittigggaagalaaaaagittciggagg	2581 2581	Qy Db
2580 2580	agtggtctcattcataaagtggaatggtagctgccaggggctggagggag	2521 2521	дb
2520 2520	ttatactaaatgaaatatgccagtcacggaaggacagattctcttgtatgaggtactcag 	2461 2461	Po de
4 4	acacaaaccatgaagtattcacccttaaagtcagacacacg 	4 4	Qy dd
2400 2400	ttcatactagccaaaaggtggtggcagcccccgtgtccattgatagatgaatgggtaaac 	2341 2341	Qy Db
34	 CTCTGAAGC	N	Db
34	aagactotgaagooggaacttaagcatgtattoatacatocatgttoacagcagtato	28	Оу
2280 2280	gatteteaaaaaaagaattaeggeataateeageaatgeeaettetggatatataecea 	2221 2221	Qy Db
2220 2220	gaaaaagtgttaatggagggcactgtaaaatggtgcagccactatggaaaacaggatgag 	2161 2161	Oy Db
2160 2160	atacactaaataaagcatgcaaaaattytygagcaaatattttaagtttttcaaaagcct 	2101 2101	ρb
2100 2100	aagttcaaataggttatttcaaaaaatgttggtagagaacatggaaaggcttttctgtac 	2041 2041	Qy
2040 2040	gagccacctcgcccagccagttcactgacactttaaacaatataacacattttcctaaaaa 	1981 1981	Qy Db
1980 1980	gaactcctgacctcaagtgatctgcccaccttggcctcccaaagtgctgggattacaggt	1921 1921	Qy Db
1920 1920	aattttttttyttattttcaggagagacaaaagtttaatcatgtgggccaggctggttt	1861 1861	Qy Db
1860 1860	tgattctcatgcctcagcctcccgagtagcttggattacaggcgatttttttt	1801 1801	Oy Db
1800 1800	goggctggagtgcactggtgtgatgttggctcactgcaacctccacctccacgctcaag.	5 1741	Db
Ę	CC 11:03:14 2001	541 agataa - 41 AGATAA;	481 cagcc- 481 CAGCC

3901 attatgttgccgaggctggtcttgaactcgtggcttcnagcagtcctcctgccttggcct 3960	Qy
3841 actytagycacatyccaccatygccayctaattttttattttttttgtagayacayaytctc 3900 	D Qy
3781 aacagcctctacctcccaggttcaagaaatcttctcaccttagcttcccgagtagctggg 3840	Qy Db
3721 ttgagacagagtettgetetgteteeeaggetggagtgcagtgacetgacgatagettae 3780 	Ωy
3661 toatotttotaaottocagtacoagootaattttgttatttttattattattattattatt 3720 	Qу
3601 tgtgcaaaagactttccattttgttgcataacgtaggaagctttggttttacttttccta 3660 	ОУ
3541 actaatattcttaattcaaaaagacattttatcacaaaagaagacaaatacttagaaaat 3600 	Оу
4 4	Qy Db
4 4	ОУ
in in	Оy
ωω	Qy Db
3241 ccacttgagagctatgctcttgcagctactcagctctgctattgcagtgcaaaagcagct 3300	Qy Db
3181 acacatctaatgcaaagatcagccacctttttctgtaaaggatctgatggtaaacatttt 3240 	Ωy
3121 ttccccttctttaaaaatagatcgatgtcttagggtgggaattaggcttcctgggcg 3180 	Оy
3061 atggattetteaaataaettageeaegggtgggataagggacetaettagtaagtatttt 3120 	ОУ
3001 agcaaacaaaaaaacagttaagattttttttttttttaaatgattcagtggaaataga 3060 	Оу
2941 gatecagecactgcaetecagectgggegacagageaagactecgteteaaacaaaaca	Оу
2881 toggggggttgagggagagagagtgggttgaacctgggaggcggagcttgcagtgagctga 2940 	Qy Db
	Db

State To Sta	S TOTO
tggagcagctggtcctaacatatcagccggagaggaaagactgacactgggagtggctgg 5040 	· 60
21 actggaagagcatctcccagaggttctgatggctgctccctctcctgcagattgactcta 4980 	Oy 49
aggeca 492 AGGECA 492	• Db 48
98	Qy 48 Db 48
tgtgggatgcaggcag 480 TGTGGGATGCAGGCAG 480	Qy 47. Db 47
1 tgccctggccccttggggttcttgtctgtcctcttcctgttgctcaagtcttccttc	0 68 Db 468
1 gtggttctaggtgaaagcgacaggtggccctggtgactgccgtggccctctctct	Qy 462 Db 462
1 gtaccgagcagcggattccagtttctgggaaatagcagaccatggccaggcaagtgtgtg 402 [ОУ 456 Db 456
ggtgtggdagctctaccccggagaa 456	Qy 450 Db 450
ggcagtgcataccegggagctactcc 450	Qy 444 Db 444
GCCGCCTCTTTCTGGTCCCTTCAGTA 444	Qy 438 Db 438
acattlacctctgaccctggcagcccactggcattgcttgfgg	Qy 432 Db 432
gccagaagggccccagccatcctagatggagccacaagtaccagtgccaaggctcttggt 432	Q 261 Db 4261
. ggaaacagtggctaaatttggggattgcagtggggcgaggcagggtgcaggggcagaggg 4260 	Qy 4201 Db 4201
caatggcagagatggagccccaagagaatactcagctttaacccaaggtgttgacaggtt 420 	Qy 4141 Db 4141
9 414 G 414	Qy 4081 Db 4081
tataagtgtgtgaaggtcatgatcagaactgccatatattttggcgggaaaatctatcac 4080 	Qy 4021 Db 4021
cccaaagtgttgggattacaggcataagccactgctcccagccttatttcgtatatttac 4020	Qy 3961 Db 3961
NAGCAGTCCTCCTGCCTTGGCCT 396	Db 3901

6061 taagagatggcattagagggagcccagtctggatgtggacttggatgccctgtgggtatc 6120 	Qy
6001 ccagcaccccagtgcagctcgtgattggaaactcaccatcggcaggca	Qy Db
5941 ttctagatgccactcccaaatccccttcatacccaccaggatgtgtgcccagccag	Qу
atc 594 ATC 594	Qу
C 588	Qу Дъ
5761 ctgcacactcagtttctctcgttttccttagttatcagtcctgtcctgtcccactcaggt 5820 	Qy Db
576 576	Db Qy
0	ОУ
564	Ф
tg 558 558	Qу
5461 ccagcactgacccatagagggctcctctcagatgggcagcagcttggagcaggccaggca 5520 [Qy Db
401 ctcgggtccctagatttaaccatggcactgaggtgccgtgtgacggtggccttggaggac 546	ОУ
341 ggggatgggaatgacttcctcgagaccatacagccaggaaatagcggtgaatctagtgat 540 	Qy Db
	Ωу
5221 cccataataagttcctaaagcatgggatctcatcgaataagactcatcatttaatccttg 5280 	Qy
5161 agccacctgtcacctctgttccccagccctttggatgtgatggtacacagtgggtgg	9 4
5101 cttttcagaaagacggcgttggcctccttcctccctgctgtttgctgagatttttcttacat 5160	Qу
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FOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6301 ACTGGTTAATTAAACTTTAATTGCTCACTGTCCACTTTTGTGCTGAATTGGAGCCTCTCTT 6360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6241 TGCTTATTCAGTCCTTCAGCTCACGGAAGGGATGCTAGTCCGTGAAGGTGACCTCACAGT 6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6241 tgcttattcagtccttcagctcacggaagggatgctagtccgtgaagggtgacctcacagt 6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6181 GCCTCAGTGAGCCCATCTGCACAGTGGGGAGCATGGAGGGATGGGTTTGGCCTGTGCTTC 6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6421 aatgatccatttcatatttttccacactgggaaggaaattgtgattggtccattcagcag 6480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6361 TGACCTCTTTCTAGCATAGAAATGGCAGCTTCTGGTACCGAAATGTTAAGGTAACATTTT 6420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6361 tgacctctttctagcatagaaatggcagcttctggtaccgaaatgttaaggtaacatttt 6420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6181 gcctcagtgagcccatctgcacagtggggagcatggagggatgggtttggcctgtgcttc 6240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 166308)
Heilig,R., Petit,J.L., Vico,V., Dasilva,C., Robert,C., Wincker,P.,
Brottier,P., Cattolico,L., Barbe,V., Pelletier,E., Artiguenave,F.,
Levy,M., Eckenberg,R., Bruls,T., deBerardinis,V., Cruaud,C.,
Gyapay,G., Saurin,W. and Weissenbach,J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CNS01DX2 166308 bp
Human chromosome 14 D
                                                                                                                                                                                                                                                                                                                                                                                                 Web : www.genoscope.cns.fr)
On Apr 3, 2001 this sequence version replaced gi:12274871
.....Genome Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (26-APR-2001) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (B-mail : seqrefégenoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                 The following BAC sequence is oriented from the T7 to the SP6 end. Upstream BAC (overlapping the T7 end): R-1070N10 Downstream BAC (overlapping the SP6 end): R-185P18 (AC-AL133167)
                                                                                                                                                                                                                                                                                                      web site: http://www.genoscope.cns.fr/
Contact: SeqRef@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                          Center: Genoscope / Centre National de Sequencage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequencing of the human chromosome 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AL139020.5 GI:13539193
                                                              Overall quality chart
                                                                                                                                    Assembly program: Phrap; version 2.0 Quality coverage: 6.03x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                          Center code: GS
                                            Range
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (bases 1 to 166308)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                chromosome 14 of Homo sapiens (Human), complete sequence.
9
                                                 bases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA sequence BAC R-164H13 of library RPCI-11
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FEATURES
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                                                                                                                                                                                                                                                                                                                                                        Matches 6473; Conservative
                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                           22901 TOCTCCTCCTCCCCCTCCTCCCCGACTGGCCCCGACTGCCCAACTGCCGGCCCCGAAC 22960
                                        23021 AAGCTACACGTGTGAGCCTAGAGGCGGGTCCCGGTTGCAGACTTGCCATGGCCTCCGAAG 23080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               source
                                                                                                                                                                                                 22961 TGCCGGCCCGGGCCCCACCCACGCGGAGCTGCTCCATTTAAGGAGATTGCGCAGCTGGA 23020
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STS
                                                                                                                                                             121
241 aagatgaggagggagaacctgggtgactgtggtcgtgcggttcaatccctcgcgtaggg 300
                                                                                                                                                                                                                  61 tgccggcccgggcccacccacgccggagctgctccatttaaggagattgcgcagctgga 120
                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                 1 teeteeteeteeceeteeteeceegaetggcacegeeceaetgeeggeecegeeeae 60
                                                                                                                                            aagctacacgtgtgagcctagaggcgggtcccggttgcagacttgccatggcctccgaag 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percentage of bases with a quality value >= 40 : 99 %.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Identified using the e-PCR software (G. Schuler)" 46913 a 36249 c 37941 g 45205 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       dbSTS:STS38175
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RHdb:RH45107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RHdb: RH7782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         dbsrs:srs38605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RHdb:RH45537
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="RPCI-11"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="matching EMBL:X82240
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                                                                                                                                                                                                                                                                                                                                                    99.3%; Score 6443.8; DB 9; 99.8%; Pred. No. 0; ative 0; Mismatches 13;
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                                                                                                                                                                                                                                                                                                                                                          13; Indels
                                                                                                                                                                                                                                                                                                                                                                                              Length 166308;
                                                                                                                                                                                                                                                                                                                                                            2; Gaps
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